RAW SEQUENCE LISTING   DATE: 05/23/2001
PATENT APPLICATION: **US/09/851,873**   TIME: 13:14:10

Input Set : **A:\00233.txt**
Output Set: **C:\CRF3\05232001\I851873.raw**

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   4 <110> APPLICANT: Kletzien, Rolf F
   5        Reardon, Ilene M
   6        Weiland, Katherine L
   8 <120> TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
  10 <130> FILE REFERENCE: 28341/00233
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/851,873
C--> 13 <141> CURRENT FILING DATE: 2001-05-08
  15 <160> NUMBER OF SEQ ID NOS: 105
  17 <170> SOFTWARE: PatentIn Ver. 2.0
  19 <210> SEQ ID NO: 1
  20 <211> LENGTH: 1026
  21 <212> TYPE: DNA
  22 <213> ORGANISM: Homo sapien
  24 <220> FEATURE:
  25 <221> NAME/KEY: CDS
  26 <222> LOCATION: (1)..(372)
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  30 Met Ala Asp Glu Lys Pro Ser Asn Gly Val Leu Val His Met Val Lys
  31  1               5                  10                  15
  33 ttg ctg atc aag acc ttt cta gat ggc att ttt gat gat ttg atg gaa    96
  34 Leu Leu Ile Lys Thr Phe Leu Asp Gly Ile Phe Asp Asp Leu Met Glu
  35              20                  25                  30
  37 aat aat gtg tta aat aca gat gag ata cac ctt ata gga aaa tgt cta   144
  38 Asn Asn Val Leu Asn Thr Asp Glu Ile His Leu Ile Gly Lys Cys Leu
  39          35                  40                  45
  41 aag ttt gtg gtg agc aat gct gaa aac ctg gtt gat gat atc act gag   192
  42 Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
  43      50                  55                  60
  45 aca gct caa att gca ggc aaa ata ttt agg gaa cac ctg tgg aat tcc   240
  46 Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
  47  65                  70                  75                  80
  49 aaa aaa cag ctg agt tca gat ata tcc agt gat gga gaa aga gag gcg   288
  50 Lys Lys Gln Leu Ser Ser Asp Ile Ser Ser Asp Gly Glu Arg Glu Ala
  51                  85                  90                  95
  53 aac atg cct ggc ctc aac atc cgc aac aaa gaa ttc aac tat ctt cat   336
  54 Asn Met Pro Gly Leu Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu His
  55              100                 105                 110
  57 aat cga aat ggt tct gaa ctt gac ctt ttg ggg atg tgagatctac        382
  58 Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met
  59          115                 120
  61 ttgaaaacct tggatactca gtggttataa aagagaatct cacagctcag gaaatggaaa   442
  63 cagcactaag gcagtttgct gctcacccag agcaccagtc ctcagacagc acattcctgg   502
  65 tgtttatgtc acatagcatc ctgaatggaa tctgtgggac caagcactgg gatcaagagc   562
  67 cagatgttct tcacgatgac accatctttg aaattttcaa caaccgtaac tgccagagtc   622
  69 tgaaagacaa acccaaggtc atcatcatgc aagcctgccg aggcaatggt gctgggattg   682
  71 tttggttcac cactgacagt ggaaaagcca gtgcagatac tcatggtcgg ctcttgcaag   742
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RAW SEQUENCE LISTING   DATE: 05/23/2001
PATENT APPLICATION: **US/09/851,873**   TIME: 13:14:10

Input Set : **A:\00233.txt**
Output Set: **C:\CRF3\05232001\I851873.raw**

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73 gtaacatctg taatgatgct gttacaaagg ctcatgtgga aaaggacttc attgctttca 802
75 aatcttccac accacataat gtttcttgga gacatgaaac aaatggctct gtcttcattt 862
77 cccaaattat ctactacttc agagagtatt cttggagtca tcatctagag gaaattttc 922
79 aaaaggttca acattcattt gagacccccaa atatactgac ccagctgccc accattgaaa 982
81 gactatccat gacacgatat ttctatctct ttcctgggaa ttaa          1026
84 <210> SEQ ID NO: 2
85 <211> LENGTH: 124
86 <212> TYPE: PRT
87 <213> ORGANISM: Homo sapiens
89 <400> SEQUENCE: 2
90 Met Ala Asp Glu Lys Pro Ser Asn Gly Val Leu Val His Met Val Lys
91  1               5                  10                  15
93 Leu Leu Ile Lys Thr Phe Leu Asp Gly Ile Phe Asp Asp Leu Met Glu
94              20                  25                  30
96 Asn Asn Val Leu Asn Thr Asp Glu Ile His Leu Ile Gly Lys Cys Leu
97              35                  40                  45
99 Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
100         50                  55                  60
102 Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
103 65              70                  75                  80
105 Lys Lys Gln Leu Ser Ser Asp Ile Ser Ser Asp Gly Glu Arg Glu Ala
106              85                  90                  95
108 Asn Met Pro Gly Leu Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu His
109              100                 105                 110
111 Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met
112         115                 120
115 <210> SEQ ID NO: 3
116 <211> LENGTH: 1026
117 <212> TYPE: DNA
118 <213> ORGANISM: Homo sapiens
120 <220> FEATURE:
121 <221> NAME/KEY: CDS
122 <222> LOCATION: (1)..(1023)
123 <223> OTHER INFORMATION:
125 <220> FEATURE:
126 <221> NAME/KEY: misc_feature /
127 <222> LOCATION: (373)..(374)..(375)
128 <223> OTHER INFORMATION: n = a or t or g or c
130 <220> FEATURE:
131 <221> NAME/KEY: misc_feature
132 <222> LOCATION: (125)       /
133 <223> OTHER INFORMATION: Xaa = any amino acid or no amino acid
135 <400> SEQUENCE: 3
136 atg gct gat gag aaa cca tcc aac ggt gtt ctg gtc cac atg gtg aag   48
137 Met Ala Asp Glu Lys Pro Ser Asn Gly Val Leu Val His Met Val Lys
138  1               5                  10                  15
140 ttg ctg atc aag acc ttt cta gat ggc att ttt gat gat ttg atg gaa   96
141 Leu Leu Ile Lys Thr Phe Leu Asp Gly Ile Phe Asp Asp Leu Met Glu
142              20                  25                  30
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RAW SEQUENCE LISTING   DATE: 05/23/2001
PATENT APPLICATION: US/09/851,873   TIME: 13:14:10

Input Set : A:\00233.txt
Output Set: C:\CRF3\05232001\I851873.raw

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    144 aat aat gtg tta aat aca gat gag ata cac ctt ata gga aaa tgt cta   144
    145 Asn Asn Val Leu Asn Thr Asp Glu Ile His Leu Ile Gly Lys Cys Leu
    146         35              40              45
    148 aag ttt gtg gtg agc aat gct gaa aac ctg gtt gat gat atc act gag   192
    149 Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
    150     50              55              60
    152 aca gct caa att gca ggc aaa ata ttt agg gaa cac ctg tgg aat tcc   240
    153 Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
    154 65              70              75              80
    156 aaa aaa cag ctg agt tca gat ata tcc agt gat gga gaa aga gag gcg   288
    157 Lys Lys Gln Leu Ser Ser Asp Ile Ser Ser Asp Gly Glu Arg Glu Ala
    158             85              90              95
    160 aac atg cct ggc ctc aac atc cgc aac aaa gaa ttc aac tat ctt cat   336
    161 Asn Met Pro Gly Leu Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu His
    162         100             105             110
W--> 164 aat cga aat ggt tct gaa ctt gac ctt ttg ggg atg nnn gat cta ctt   384
W--> 165 Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met Xaa Asp Leu Leu
    166         115             120             125
    168 gaa aac ctt gga tac tca gtg gtt ata aaa gag aat ctc aca gct cag   432
    169 Glu Asn Leu Gly Tyr Ser Val Val Ile Lys Glu Asn Leu Thr Ala Gln
    170     130             135             140
    172 gaa atg gaa aca gca cta agg cag ttt gct gct cac cca gag cac cag   480
    173 Glu Met Glu Thr Ala Leu Arg Gln Phe Ala Ala His Pro Glu His Gln
    174 145             150             155             160
    176 tcc tca gac agc aca ttc ctg gtg ttt atg tca cat agc atc ctg aat   528
    177 Ser Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Ser Ile Leu Asn
    178             165             170             175
    180 gga atc tgt ggg acc aag cac tgg gat caa gag cca gat gtt ctt cac   576
    181 Gly Ile Cys Gly Thr Lys His Trp Asp Gln Glu Pro Asp Val Leu His
    182         180             185             190
    184 gat gac acc atc ttt gaa att ttc aac aac cgt aac tgc cag agt ctg   624
    185 Asp Asp Thr Ile Phe Glu Ile Phe Asn Asn Arg Asn Cys Gln Ser Leu
    186         195             200             205
    188 aaa gac aaa ccc aag gtc atc atc atg caa gcc tgc cga ggc aat ggt   672
    189 Lys Asp Lys Pro Lys Val Ile Ile Met Gln Ala Cys Arg Gly Asn Gly
    190     210             215             220
    192 gct ggg att gtt tgg ttc acc act gac agt gga aaa gcc agt gca gat   720
    193 Ala Gly Ile Val Trp Phe Thr Thr Asp Ser Gly Lys Ala Ser Ala Asp
    194 225             230             235             240
    196 act cat ggt cgg ctc ttg caa ggt aac atc tgt aat gat gct gtt aca   768
    197 Thr His Gly Arg Leu Leu Gln Gly Asn Ile Cys Asn Asp Ala Val Thr
    198             245             250             255
    200 aag gct cat gtg gaa aag gac ttc att gct ttc aaa tct tcc aca cca   816
    201 Lys Ala His Val Glu Lys Asp Phe Ile Ala Phe Lys Ser Ser Thr Pro
    202         260             265             270
    204 cat aat gtt tct tgg aga cat gaa aca aat ggc tct gtc ttc att tcc   864
    205 His Asn Val Ser Trp Arg His Glu Thr Asn Gly Ser Val Phe Ile Ser
    206         275             280             285
    208 caa att atc tac tac ttc aga gag tat tct tgg agt cat cat cta gag   912
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209 Gln Ile Ile Tyr Tyr Phe Arg Glu Tyr Ser Trp Ser His His Leu Glu
210     290             295             300
212 gaa att ttt caa aag gtt caa cat tca ttt gag acc cca aat ata ctg     960
213 Glu Ile Phe Gln Lys Val Gln His Ser Phe Glu Thr Pro Asn Ile Leu
214 305             310             315             320
216 acc cag ctg ccc acc att gaa aga cta tcc atg aca cga tat ttc tat    1008
217 Thr Gln Leu Pro Thr Ile Glu Arg Leu Ser Met Thr Arg Tyr Phe Tyr
218             325             330             335
220 ctc ttt cct ggg aat taa                                            1026
221 Leu Phe Pro Gly Asn
222             340
225 <210> SEQ ID NO: 4
226 <211> LENGTH: 341
227 <212> TYPE: PRT
228 <213> ORGANISM: Homo sapiens
230 <220> FEATURE:
231 <221> NAME/KEY: misc_feature
232 <222> LOCATION: 125
233 <223> OTHER INFORMATION: Xaa = any amino acid or no amino acid
235 <400> SEQUENCE: 4
236 Met Ala Asp Glu Lys Pro Ser Asn Gly Val Leu Val His Met Val Lys
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239 Leu Leu Ile Lys Thr Phe Leu Asp Gly Ile Phe Asp Asp Leu Met Glu
240             20              25              30
242 Asn Asn Val Leu Asn Thr Asp Glu Ile His Leu Ile Gly Lys Cys Leu
243         35              40              45
245 Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
246     50              55              60
248 Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
249 65              70              75              80
251 Lys Lys Gln Leu Ser Ser Asp Ile Ser Ser Asp Gly Glu Arg Glu Ala
252             85              90              95
255 Asn Met Pro Gly Leu Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu His
256             100             105             110
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W-->
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258 Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met Xaa Asp Leu Leu
259         115             120             125
261 Glu Asn Leu Gly Tyr Ser Val Val Ile Lys Glu Asn Leu Thr Ala Gln
262     130             135             140
264 Glu Met Glu Thr Ala Leu Arg Gln Phe Ala Ala His Pro Glu His Gln
265 145             150             155             160
268 Ser Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Ser Ile Leu Asn
269             165             170             175
271 Gly Ile Cys Gly Thr Lys His Trp Asp Gln Glu Pro Asp Val Leu His
272             180             185             190
274 Asp Asp Thr Ile Phe Glu Ile Phe Asn Asn Arg Asn Cys Gln Ser Leu
275         195             200             205
277 Lys Asp Lys Pro Lys Val Ile Ile Met Gln Ala Cys Arg Gly Asn Gly
278     210             215             220
280 Ala Gly Ile Val Trp Phe Thr Thr Asp Ser Gly Lys Ala Ser Ala Asp
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RAW SEQUENCE LISTING   DATE: 05/23/2001
PATENT APPLICATION: US/09/851,873   TIME: 13:14:10

Input Set : A:\00233.txt
Output Set: C:\CRF3\05232001\I851873.raw

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281 225                     230·              235               240
283 Thr His Gly Arg Leu Leu Gln Gly Asn Ile Cys Asn Asp Ala Val Thr
284             .           245               250               255
286 Lys Ala His Val Glu Lys Asp Phe Ile Ala Phe Lys Ser Ser Thr Pro
287             260               265               270
289 His Asn Val Ser Trp Arg His Glu Thr Asn Gly Ser Val Phe Ile Ser
290             275               280               285
292 Gln Ile Ile Tyr Tyr Phe Arg Glu Tyr Ser Trp Ser His His Leu Glu
293         290               295               300
295 Glu Ile Phe Gln Lys Val Gln His Ser Phe Glu Thr Pro Asn Ile Leu
296 305               310               315               320
298 Thr Gln Leu Pro Thr Ile Glu Arg Leu Ser Met Thr Arg Tyr Phe Tyr
299             325               330               335
301 Leu Phe Pro Gly Asn
302             340
305 <210> SEQ ID NO: 5
306 <211> LENGTH: 915
307 <212> TYPE: DNA
308 <213> ORGANISM: Homo sapiens
310 <220> FEATURE:
311 <221> NAME/KEY: CDS
312 <222> LOCATION: (1)..(372)
318 <400> SEQUENCE: 5
319 atg gct gat gag aaa cca tcc aac ggt gtt ctg gtc cac atg gtg aag      48
320 Met Ala Asp Glu Lys Pro Ser Asn Gly Val Leu Val His Met Val Lys
321  1               5                  10                  15
323 ttg ctg atc aag acc ttt cta gat ggc att ttt gat gat ttg atg gaa      96
324 Leu Leu Ile Lys Thr Phe Leu Asp Gly Ile Phe Asp Asp Leu Met Glu
325             20                  25                  30
327 aat aat gtg tta aat aca gat gag ata cac ctt ata gga aaa tgt cta     144
328 Asn Asn Val Leu Asn Thr Asp Glu Ile His Leu Ile Gly Lys Cys Leu
329             35                  40                  45
331 aag ttt gtg gtg agc aat gct gaa aac ctg gtt gat gat atc act gag     192
332 Lys Phe Val Val Ser Asn Ala Glu Asn Leu Val Asp Asp Ile Thr Glu
333     50                  55                  60
335 aca gct caa att gca ggc aaa ata ttt agg gaa cac ctg tgg aat tcc     240
336 Thr Ala Gln Ile Ala Gly Lys Ile Phe Arg Glu His Leu Trp Asn Ser
337 65                  70                  75                  80
339 aaa aaa cag ctg agt tca gat ata tcc agt gat gga gaa aga gag gcg     288
340 Lys Lys Gln Leu Ser Ser Asp Ile Ser Ser Asp Gly Glu Arg Glu Ala
341             85                  90                  95
343 aac atg cct ggc ctc aac atc cgc aac aaa gaa ttc aac tat ctt cat     336
344 Asn Met Pro Gly Leu Asn Ile Arg Asn Lys Glu Phe Asn Tyr Leu His
345             100               105               110
347 aat cga aat ggt tct gaa ctt gac ctt ttg ggg atg tgagatctac          382
348 Asn Arg Asn Gly Ser Glu Leu Asp Leu Leu Gly Met
349             115               120
351 ttgaaaacct tggatactca gtggttataa aagagaatct cacagctcag gaaatggaaa   442
353 cagcactaag gcagtttgct gctcacccag agcaccagtc ctcagacagc acattcctgg   502
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Please Note:
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.**

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/851,873**

DATE: 05/23/2001
TIME: 13:14:11

Input Set : **A:\00233.txt**
Output Set: **C:\CRF3\05232001\I851873.raw**

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:494 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:498 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:535 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:582 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1024 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1030 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1033 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1036 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1078 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1087 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1091 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:1125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:1128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:1157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:1160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:1537 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:1578 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55